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QY      160 NGVTTTRVYDCCCKASCSMPKANKVSSPVKSCMKOGVTAL-SISNINQSGCNGSNSTVYCNQD 218
Db      16  SGRTTRVYDCCCKASCAWEKKAALVTPDYCTCKDGTTRVASNIDTVKSAACDGGEGVYCYDOA 75

QY      219 PMATNDNLAYEPAAAALISGGESRWCSCSEFLTFSTSTVAKKKWVIQVNTNGGDLGSSTG 278
Db      76  PMAVNDISVAYVFPAAAACC-GGESGACNCCYELTFTSGVNEKRWQVNTNGGDLGSSN-- 132

QY      279 AHFDLQMPGGGCVGI-FNGCSXOMGAPNDMDGSRVYGGISASDSCSLSPALQAGCKKRFPMWF 338
Db      133 -QFDLAPFGGGVGIYNGCTQOQSGAPADDMGSRVGGVSSRSRSECSQLPSEGLQAGCKKRFPMWF 191

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OY 339 KNAADNPSMTYKVTCPKEITAKTGCGR 365
 DB 192 QNADNPSINFNOVTPGELTAKTNCKR 218

RESULT 2

O9P868 PRELIMINARY; PRT; 410 AA.
 ID 09P868
 AC 09P868
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Endoglucanase 45A.
 GN CEL45A.
 OS Pirmomyces equi.
 OC Eukaryota; Fungi; Chytridiomycota; Neocallimastixales;
 OC Neocallimastixaceae; Pirmomyces.
 OX NCBI_TaxID=99929;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20391845; PubMed=10931904;
 RA Eberhardt R.Y., Gilbert H.J., Hazlewood G.P.;
 RT "Primary sequence and enzymatic properties of two modular
 endoglucanases, Cel5A and Cel45A, from the anaerobic fungus Pirmomyces
 equi.";
 RL Microbiology 146:1999-2008 (2000).
 DR EMBL; AJ277482; CAB92325.1; -.
 DR HSSP; P43316; 2ENG.
 DR InterPro; IPR002883; CBD 5.
 DR InterPro; IPR000334; GH 45.
 DR Pfam; PF02013; CBM_10; 3.
 DR Pfam; PF02015; Glyco_hydro_45; 1.
 DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1
 SQ SEQUENCE 410 AA; 44380 MM; DB13BD9CFD8238DC CRC64;

Query Match 38.6%; Score 779.5; DB 3; Length 410;
 Best Local Similarity 40.7%; Pred. No. 3.6e-46;
 Matches 168; Conservative 52; Mismatches 116; Indels 77; Gaps 14;

OY 12 LALALGTEMASAKCSKLYGCGGKDMNGPTCCSGSTCYVSN----- 54
 DB 1 MRALITSCIALAASIAKSAACMAQS--QGVNCCNPPSTVEYTDASGQGVNGWCGI 59
 OY 55 DY-YSGCLAPES-NGNKSSECSKLYGCGGKDMNGPTCCSGSTCYVSN DYSGCLAPES 112
 DB 60 DYSGQONQNESCTGNSGYPCCNTC-QATYTDGQDMAFENGWNGIKNSCKQO---PON 115
 OY 113 NGNKTSESAHKTYYY-----TAPAKEITTTAKASNSSSG 148
 DB 116 NNQCTGNGAYRCNCQTATYTDNEGKMAFENGWNGIKYSCPSQOVTTTRTTTQQ 175
 OY 149 KSIYSGGASG-----NGVTTRYMDCKKASCSMPGKA---NVSFVKSCKNDGV 194
 DB 176 QOPTSGGGGNSVPLNPPPSGGTGTTRTYMDCCLASGQNGCNKNDAGQGVVRCNDGI 235
 OY 195 TALSD-SN---VSGGCGNSGYMCDNDOPMAVNDLAVGPAALISGGSESRMCCSEEL 250
 DB 236 TPTTDLNLMRYVSGGNSGYMCDNDOPMAVNDLAVGPAALISGGSESRMCCSEEL 288
 OY 251 TPTTSTVAKKAVIQVTTNGDLSSTGAHFDLQWPGGSGVGFNGCSKQMGAPNDGMSR 310
 DB 289 KPTSGIADKQMTIVQTTNGDLSN--HFDIQMGGSGFGIFDCTGQFGSGSYQ-WGER 344
 OY 311 YGSISSADCSLPSALQAGCKRFPNADNPSMTYKVTCPKEITAKTGC 363
 DB 345 YGSISSASQCANLPQKAGCKRFPNADNPSMTYKVTCPKEITAKTGC 397

RESULT 3
 ID 09JH84 PRELIMINARY; PRT; 220 AA.
 AC 09JH84

DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Family 45 cellulase homologue.
 OS unclassified eukaryotes.
 OC Eukaryota.
 OX NCBI_TaxID=42452;
 RN
 RP SEQUENCE FROM N.A.
 RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
 RT "Diverse genes of family 45 cellulase homologues of the symbiotic
 RT protists in the hindgut of termite Reticulitermes speratus";
 RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AB045179; BAA98049.1; -.
 DR HSSP; P43316; 2ENG.
 DR InterPro; IPR000334; GH 45.
 DR Pfam; PF02015; Glyco_hydro_45; 1.
 DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
 SQ SEQUENCE 220 AA; 23274 MM; 26AF5357512EA061 CRC64;

Query Match 38.5%; Score 778.5; DB 14; Length 220;
 Best Local Similarity 64.2%; Pred. No. 2.2e-46;
 Matches 138; Conservative 31; Mismatches 41; Indels 5; Gaps 3;

OY 152 IVSGASGNGVTRRYMDCKKASGWPGRKANVSPYKSCNKDGVTAL-SDSNVQSGCNGN 210
 DB 9 LISWLVGDSGRTTRRYMDCKKASGWPGRKANVSPYKSCNKDGVTAL-SDSNVQSGCNGN 68
 OY 211 SYMCDNQPAVNDNLAVGFAAALISGGSESRMCCSEELTTSVAKKAVIQVNTNG 270
 DB 69 GYMCTYDQPAVAVNDVSVAGFAAACC-GGETGACCCCYELTFISGVNKKRNVQVNTNG 127
 OY 271 GDLCSSTGAHPDLQWPGGSGVGFNGCSKQMGAPNDGMSRYGSISSADCSLPSALQAG 330
 DB 128 GDLCSN--QFDLAPGSGVGIYNGCTQSGAPADGMSRYGSISSADCSLPSALQAG 184
 OY 331 CKRFPNFKNADNPSMTYKVTCPKEITAKTGCGR 365
 DB 185 CKRFPNFKNADNPSINFNOVTPGELTAKTNCKR 219

RESULT 4

O9JH91 PRELIMINARY; PRT; 219 AA.
 ID 09JH91
 AC 09JH91
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Family 45 cellulase homologue.
 OS unclassified eukaryotes.
 OC Eukaryota.
 OX NCBI_TaxID=42452;
 RN
 RP SEQUENCE FROM N.A.
 RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
 RT "Diverse genes of family 45 cellulase homologues of the symbiotic
 RT protists in the hindgut of termite Reticulitermes speratus";
 RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AB045172; BAA98042.1; -.
 DR HSSP; P43316; 2ENG.
 DR InterPro; IPR000334; GH 45.
 DR Pfam; PF02015; Glyco_hydro_45; 1.
 DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
 SQ SEQUENCE 219 AA; 23126 MM; A712EF3F3CAB041C CRC64;

Query Match 38.5%; Score 777.5; DB 14; Length 219;
 Best Local Similarity 64.7%; Pred. No. 2.6e-46;
 Matches 139; Conservative 30; Mismatches 41; Indels 5; Gaps 3;

OY 152 IVSGASGNGVTRRYMDCKKASGWPGRKANVSPYKSCNKDGVTAL-SDSNVQSGCNGN 210
 DB 8 LISWLVGDSGRTTRRYMDCKKASGWPGRKANVSPYKSCNKDGVTAL-SDSNVQSGCNGN 67

Oy	211	SYNCINNOPAAVNDLNATYFAAALASGGGSESMCCSCELEFETSTSVAGKKGVQVNTTG	270
Db	68	GTYCTDQAPPAVNDVSAYTGPAAAAACC-GGESACCNCTELTFETSPVGKRMVVQVNTTG	126
Oy	271	GDDGSSTGAHFDLQMPGGGVGI-FNGCSKQWMA-PNDGMGSRJGAISSASDCSLPSALOAG	330
Db	127	GDDGSN---QFDLAIPGGGVGIYNCTQQSGAPSGMGSRRGTGYSSRSECQLPSSGLOAG	193
Oy	331	CKGRFMFKXADNPSTMTEKYEVTCPEKETAKTGCSR	365
Db	184	CQTFDFMQADNPISINFNQVTCPESLTAKTKCCR	218

ID	Q9JH87	PRELIMINARY;	PRT;	219 AA.
AC	Q9JH87			
DT	01-OCT-2000	(TREMBLrel. 15, Created)		
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)		
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)		
DE	Family 45 cellulase homologue.			
OS	unclassified eukaryotes.			
OC	Eukaryota.			
OX	NCBI_taxid=42452;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Ohoko K., Ohkuma M., Moriya S., Kudo T.;			
RT	"Diverse genes of family 45 cellulase homologues of the symbiotic prokotes in the hindgut of termite Reticulitermes speratus."			
RL	Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AB045176; BAA98046.1; -			
DR	HSSP; P43316; ZENG.			
DR	InterPro; IPR000334; GH_45.			
DR	Pfam; PF02015; Glyco_hydro_45; 1.			
DR	PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.			
SO	SEQUENCE 219 AA; 23334 MW; 4BDEF4EC9ACC772D CRC64;			
QY	Query Match	38.2%; Score 771.5; DB 14; Length 219;		
Db	Best Local Similarity	62.5%; Pred. No. 6.7e-46;		
Matches	135; Conservative	33; Mismatches	43; Indels	5; Gaps
QY	151	SIVSGASGNGVTRYPDCCRASCPGKANYSPFKSCNDGVTL-SDSIVSGCNGG	209	
Db	7	AFISLSDSGGTRYPDCCGKSCMEKKAANDKPIDCADGTRVANSNDIVSGCDGG	66	
QY	210	NSYWCNDQPNVNDNLAYGFAAALISGGESRWCCSCPELTFTSTVAGKMYQVNT	269	
Db	67	DGFMYDDTPQVSSLSYGFALAAC-C-GGSGACCGCTELTFISGPNVKKMYQVNT	125	
QY	270	GGDGLSSGTGAHFDLQMPGGGVGIFNGCSKQWGAIPNDGSGRYGJISASDSSLPALQA	329	
Db	126	GGDGLSN---QFDLAIPEGGVGIVNGCTAAGAPSDGMGSGRYGVSRSRSGQLPSGLQA	182	
QY	330	GCKRPFNFKAADNPSMTYKCYKTEIKTATGCSR	365	
Db	183	GCOMRFEDWFQADNPSINFQVSCPSSEIIAKTKCNR	218	
RESULT 6				
Q9JH83				
ID	Q9JH83	PRELIMINARY;	PRT;	220 AA.
AC	Q9JH83			
DT	01-OCT-2000	(TREMBLrel. 15, Created)		
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)		
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)		
DE	Family 45 cellulase homologue.			
OS	unclassified eukaryotes.			
OC	Eukaryota.			
OX	NCBI_taxid=42452;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Ohoko K., Ohkuma M., Moriya S., Kudo T.;			
RT	"Diverse genes of family 45 cellulase homologues of the symbiotic			

RT protectors in the hindgut of temite Reticulitermes operatus.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBP databases.
 DR EMBL; AB045157; BAA98037.1; -
 DR EMBL; AB045156; BAA98036.1; -
 DR HSSP; P43116; 2ENG
 DR InterPro; IPR000334; GH_45
 DR Pfam; PF02015; GLYCO_HYDRO_45.1.
 DR PROSITE; PS01140; GLYCOSTYL_HYDROL_F45; UNKNOWN_1.
 SQ SEQUENCE 220 AA; 23108 MW; 97738D831BCFASF3 CRC64;

Query Match	38.1%	Score 769	DB 14	Length 220
Best Local Similarity	63.3%	Pred. No. 1e-45		
Matches	138	Conservative	29	Mismatches 45; Indels 6; Gaps 4;

QY	150	YSIYSGAGSG-NGYTTTRYMDCKKASGMPGKANVSPYKSCNKQGYAL-SDSNVQSGCN	207
Db	6	PSLIAVLVFGSGGKTRTRYMDCKKSCGMEADVADSKPIDTCAKQGTTRVASNDTVKSCGD	65
QY	208	GGNSYMCNDNDPMAYVNNNLAYGFAPAAAIISGGGSRMCCSPCLFTFTSTSVAGKKIVQVT	267
Db	66	GGDGYMCTDQTPMGVNDSYALGFPAALIS-GGEIQAACCNCYELFTSPVNGKKITVQVT	124
QY	268	NTGGDLSSTGAAHFDLQMPGGGVGIPNGCSKQMGAPNDGWSRGYIGSSADCSLPBAL	327
Db	125	NTGGDLSLN---QFDLIAIPGGGVGIIYNGCTAQSGAPADGWSRBYGVSSRSECSQLPGL	181
QY	328	QAGCKWRPNFKNADNPMTYKATYCTCPKRIYAKTGCSR	365
Db	182	QAGCKWRPNFQANDNPSPNNVAVSCSEBLIAKNCRR	219

RESULT 7

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ID      Q9JH89          PRELIMINARY;       PRT;        219 AA.
AC      Q9JH89;
DT      01-OCT-2000 (TREMBLrel. 15, Created)
DT      01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT      01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE      Family 45 cellulase homologue.
OC      unclassified eukaryotes.
CC      Eukarya.
OX      NCBI_TaxID=42452;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT      "Diverse genes of family 45 cellulase homologues of the symbiotic
RL      protists in the hindgut of termite Reticulitermes speratus.";
RL      Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
DR      EMBL; AB045174; BAA98044.1; -
DR      HSSP; P43316; ZENG.
DR      InterPro; IPR000334; GH_45.
DR      Pfam; PF02015; Glyco_hydro_45; 1.
DR      PROSITE; PS01140; GLYCO_SYL_HYDROL_P45; UNKNOWN 1.
SQ      SEQUENCE   219 AA; 23033 MW; CA29SCADBF33199 CRC64;

Query Match           38.0%; Score 767.5; DB 14; Length 219;
Best Local Similarity 64.7%; Pred. No. 1.3e-45;
Matches 134; Conservative 29; Mismatches 39; Indels 5; Gaps 3.

QY      160 NGVTRWDDCKKASCSPGKRANVSPPVKSCNKDKDVTLN-SDSNVSGCGNGNSVYCNDNQ 218
         :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB      16 SGKTRRWDDCKKSGCMEKKANVKKPLDTCAKDGVTRAASNDTVKSGCDGDGFMCYDOT 75
         :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||

QY      219 PMAVNDNLAYFAFAAALISGGESRWRCSCEFLTFTSTSVAKRKAVIQVTNTGDIAGSSTG 278
         ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
         ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB      76 PMQVSDSLSYFAAALACC-GGESGACGCCCYELLTFTSGRVNKKMIVQITNTGDIAGSN-- 132
         ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||

QY      279 AHFDLQMFPGVGVI-FNGGSKQMGAIPNDWGSRVYGIISSAPDCSSLPSLAQAGCKWFNF 338
         ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB      133 -QFDLIAIFGGGVGIYNCTAAGSAIPDOWGSRVYGVSRSSECSQLPSGLQAGCQWRFDWF 191
         :|||||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY      339 KNADNPSTMYTEVATCPKEITAKTGCSR 365
         :|||||::||::||::||::||::||::||::||::||::||::||::||::||::||::||

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Db 192 QNADNPSINFNVKCPSEIIAKTNCNR 218

RESULT 8

PRELIMINARY; PRT; 217 AA.

Q9JH95
AC Q9JH95; PRELIMINARY; PRT; 217 AA.
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
proteins in the hindgut of termite Reticulitermes speratus."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045168; BAA98038.1; --
DR HSSP; P43316; ZENG.
DR InterPro; IPR000334; GH 45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
SQ SEQUENCE 217 AA; 22796 MW; 660DD1346B3769DB CRC64;

Query Match 37.8%; Score 764.5; DB 14; Length 217;
Best Local Similarity 65.2%; Pred. No. 2e-45;
Matches 135; Conservative 26; Mismatches 41; Indels 5; Gaps 3;

QY 160 NGVTRVWDCCKASCSMPKAVSSPVKSCNKGVTAL-SDSNVQSGNGNSYMCNDNQ 218
DB 14 SGKTRVWDCCKSGCEMEKAVNDKPIDTCADGTTTAVASNDTVKSGCDGGGFWCYDQT 73
QY 219 PMAVNDNLAYGFAPAAAIISGGESRWCCSFELTFTSTVAGKKMVIQVNTGDLGSGTG 278
DB 74 PMGVNDVYALGFAPAAAIIS-GGEKAAACNCYELTFTSGPVNGKMTVQVNTGDLGSGN-- 130
QY 279 AHFDLQMPGGVGIENFGCSKQMGAPNDGSRGYSASDSSLPALQAGCKRPFMF 338
DB 131 -QFDLAIPEGGVGIVNGCTAQSAGPADGWSRGGVSSRECCQLPSGLQAGCCMRPFMF 189

RESULT 9

PRELIMINARY; PRT; 219 AA.

Q9JH90
AC Q9JH90; PRELIMINARY; PRT; 219 AA.
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
proteins in the hindgut of termite Reticulitermes speratus."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045173; BAA98043.1; --
DR HSSP; P43316; ZENG.
DR InterPro; IPR000334; GH 45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
SQ SEQUENCE 219 AA; 23037 MW; 372E016415530A9A CRC64;

Query Match 37.8%; Score 763.5; DB 14; Length 219;

Best Local Similarity 64.3%; Pred. No. 2.4e-45;
Matches 133; Conservative 28; Mismatches 41; Indels 5; Gaps 3;

QY 160 NGVTRVWDCCKASCSMPKAVSSPVKSCNKGVTAL-SDSNVQSGNGNSYMCNDNQ 218
DB 16 SGKTRVWDCCKSGCEMEKAVNDKPIDTCADGTTTAVASNDTVKSGCDGGGFWCYDQT 75
QY 219 PMAVNDNLAYGFAPAAAIISGGESRWCCSFELTFTSTVAGKKMVIQVNTGDLGSGTG 278
DB 76 PMGVNDVYALGFAPAAAIIS-GGEKAAACNCYELTFTSGPVNGKMTVQVNTGDLGSGN-- 132
QY 279 AHFDLQMPGGVGIENFGCSKQMGAPNDGSRGYSASDSSLPALQAGCKRPFMF 338
DB 133 -QFDLAIPEGGVGIVNGCTAQSAGPADGWSRGGVSSRECCQLPSGLQAGCCMRPFMF 191

RESULT 10

PRELIMINARY; PRT; 220 AA.

Q9JH93
AC Q9JH93; PRELIMINARY; PRT; 220 AA.
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
proteins in the hindgut of termite Reticulitermes speratus."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045170; BAA98040.1; --
DR HSSP; P43316; ZENG.
DR InterPro; IPR000334; GH 45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
SQ SEQUENCE 220 AA; 23091 MW; 35F174F9B79C2D65 CRC64;

Query Match 37.7%; Score 762.5; DB 14; Length 220;
Best Local Similarity 65.0%; Pred. No. 2.8e-45;
Matches 134; Conservative 26; Mismatches 41; Indels 5; Gaps 3;

QY 161 GVTTRVWDCCKASCSMPKAVSSPVKSCNKGVTAL-SDSNVQSGNGNSYMCNDNQ 219
DB 18 GTRVWDCCKSGCEMEKAVNDKPIDTCADGTTTAVASNDTVKSGCDGGGFWCYDQSP 77
QY 220 PMAVNDNLAYGFAPAAAIISGGESRWCCSFELTFTSTVAGKKMVIQVNTGDLGSGTG 279
DB 78 MGVNDVYALGFAPAAAIIS-GGEKAAACNCYELTFTSGPVNGKMTVQVNTGDLGSGN-- 133
QY 280 AHFDLQMPGGVGIENFGCSKQMGAPNDGSRGYSASDSSLPALQAGCKRPFMF 339
DB 134 QFDLAIPEGGVGIVNGCTAQSAGPADGWSRGGVSSRECCQLPSGLQAGCCMRPFMF 193

RESULT 11

PRELIMINARY; PRT; 219 AA.

Q9JH88
AC Q9JH88; PRELIMINARY; PRT; 219 AA.
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Family 45 cellulase homologue.

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OS unclassified eukaryotes.
OC Eukaryota.
NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RL proteases in the hindgut of termite Reticulitermes speratus."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045175; BAA98045.1; -.
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
SQ SEQUENCE 219 AA; 23030 MM; 179BFI344C6D024 CRC64;

Query Match 37.6%; Score 759.5; DB 14; Length 219;
Best Local Similarity 64.3%; Pred. No. 4.5e-45;
Matches 133; Conservative 26; Mismatches 43; Indels 5; Gaps 3;

OY 160 NGVTRRYWDCCKASGSMFGKANNVSSPVKSCNKGVTAL-SDSNVQSGNGGNSYWCNDNQ 218
DB 16 SKGTRRYWDCCKSGCGMEKKNVDPKPIDTCAKDGTRVASNDTVASGCDGGTGYCYDT 75
OY 219 PMAVNDNLAYGFAAAAIISGGESRWCCSFELFTSTSVAGKXVIVQVNTGDLGSGSTG 278
DB 76 PMQVSDSLSYGFAAAACC-GGESGACCCGCELTFTSGPVNGKXMI VQITNTGGDLGSM-- 132
OY 279 AHFDLQMPGGVGIFNGCSKQWGA PDGWSRGYGISASDCSLPSALQAGCKRFRWF 338
DB 133 -QFDLAIFGGGVGIVNGCTSGSGAPADGWSRGYGVSSRSRSCQLPSGLQAGCQWRPWF 191
OY 339 KNAADPSMTYKEVTCPEKITAKTGCSR 365
DB 192 ANADPNINFTNVKCPSELIAKTNCR 218

RESULT 12
OY 160 NGVTRRYWDCCKASGSMFGKANNVSSPVKSCNKGVTAL-SDSNVQSGNGGNSYWCNDNQ 218
ID O9JH86 PRELIMINARY; PRT; 219 AA.
AC O9JH86;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RL proteases in the hindgut of termite Reticulitermes speratus."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045177; BAA98047.1; -.
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
SQ SEQUENCE 219 AA; 23158 MM; ECD686EABEDIDDI CRC64;

Query Match 37.5%; Score 756.5; DB 14; Length 219;
Best Local Similarity 63.3%; Pred. No. 7.2e-45;
Matches 131; Conservative 29; Mismatches 42; Indels 5; Gaps 3;

OY 160 NGVTRRYWDCCKASGSMFGKANNVSSPVKSCNKGVTAL-SDSNVQSGNGGNSYWCNDNQ 218
DB 16 SKGTRRYWDCCKSGCGMEKKNVDPKPIDTCAKDGTRVASNDTVASGCDGGTGYCYDT 75
OY 219 PMAVNDNLAYGFAAAAIISGGESRWCCSFELFTSTSVAGKXVIVQVNTGDLGSGSTG 278
DB 76 PMQVSDSLSYGFAAAACC-GGESGACCCGCELTFTSGPVNGKXMI VQITNTGGDLGSM-- 132

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OY 279 AHFDLQMPGGVGIFNGCSKQWGA PDGWSRGYGISASDCSLPSALQAGCKRFRWF 338
DB 133 -QFDLAIFGGGVGIVNGCTSGSGAPADGWSRGYGVSSRSRSCQLPSGLQAGCQWRPWF 191
OY 339 KNAADPSMTYKEVTCPEKITAKTGCSR 365
DB 192 ANADPNINFTNVKCPSELIAKTNCR 218

RESULT 13
OY 160 NGVTRRYWDCCKASGSMFGKANNVSSPVKSCNKGVTAL-SDSNVQSGNGGNSYWCNDNQ 218
ID O9JH94 PRELIMINARY; PRT; 221 AA.
AC O9JH94;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RL proteases in the hindgut of termite Reticulitermes speratus."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045169; BAA98039.1; -.
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
SQ SEQUENCE 221 AA; 23220 MM; BA84CEB0A8C46372 CRC64;

Query Match 37.4%; Score 754.5; DB 14; Length 221;
Best Local Similarity 63.3%; Pred. No. 1e-44;
Matches 131; Conservative 30; Mismatches 41; Indels 5; Gaps 3;

OY 160 NGVTRRYWDCCKASGSMFGKANNVSSPVKSCNKGVTAL-SDSNVQSGNGGNSYWCNDNQ 218
DB 17 SKGTRRYWDCCKSGCGMEKKNVDPKPIDTCAKDGTRVASNDTVASGCDGGTGYCYDT 76
OY 219 PMAVNDNLAYGFAAAAIISGGESRWCCSFELFTSTSVAGKXVIVQVNTGDLGSGSTG 278
DB 77 PMAVNDLSLGFAAAVS-GGEKKAACCGCYELTFTSGPVNGKXIVQVNTGDLGSGSM-- 133
OY 279 AHFDLQMPGGVGIFNGCSKQWGA PDGWSRGYGISASDCSLPSALQAGCKRFRWF 338
DB 134 -QFDLAIFGGGVGIVNGCTSGSGAPADGWSRGYGVSSRSRSCQLPSGLQAGCQWRPWF 192
OY 339 KNAADPSMTYKEVTCPEKITAKTGCSR 365
DB 193 ANADPNINFTNVKCPSELIAKTNCR 218

RESULT 14
OY 160 NGVTRRYWDCCKASGSMFGKANNVSSPVKSCNKGVTAL-SDSNVQSGNGGNSYWCNDNQ 218
ID O9JH85 PRELIMINARY; PRT; 218 AA.
AC O9JH85;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RL proteases in the hindgut of termite Reticulitermes speratus."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045178; BAA98048.1; -.
DR HSSP; P43316; 3ENG.

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